

# Environment-wide studies (EWAS) on Metabolic-syndrome-related phenotypes: T2D and Cholesterol

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# “Exposome”-wide measures on an epidemiological scale

What if we could define and use *exposome* as we do the *genome*?

ie, GWAS to “E”WAS



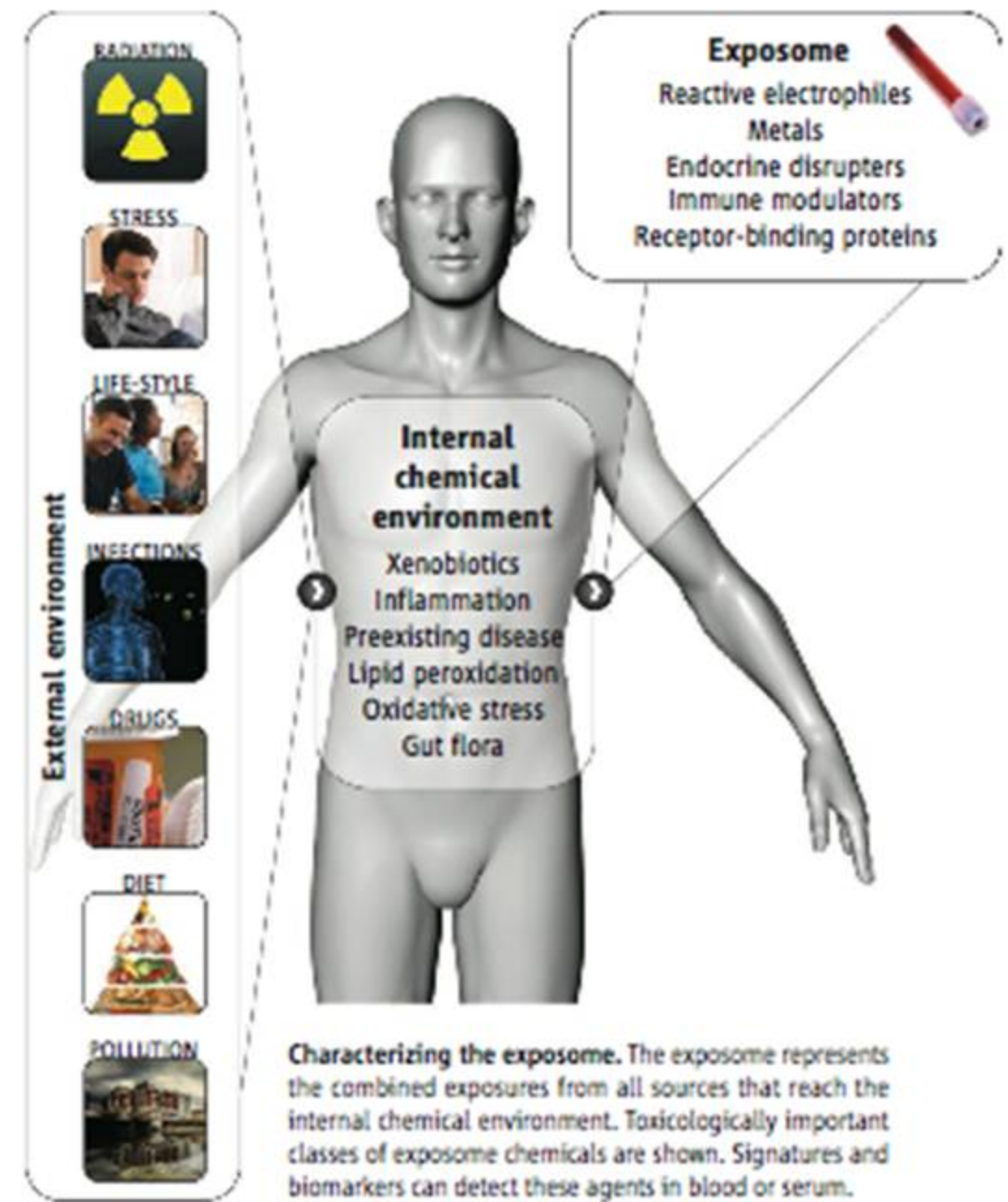
HapMap project:

<http://hapmap.ncbi.nlm.nih.gov>

/



Illumina “variant chip”

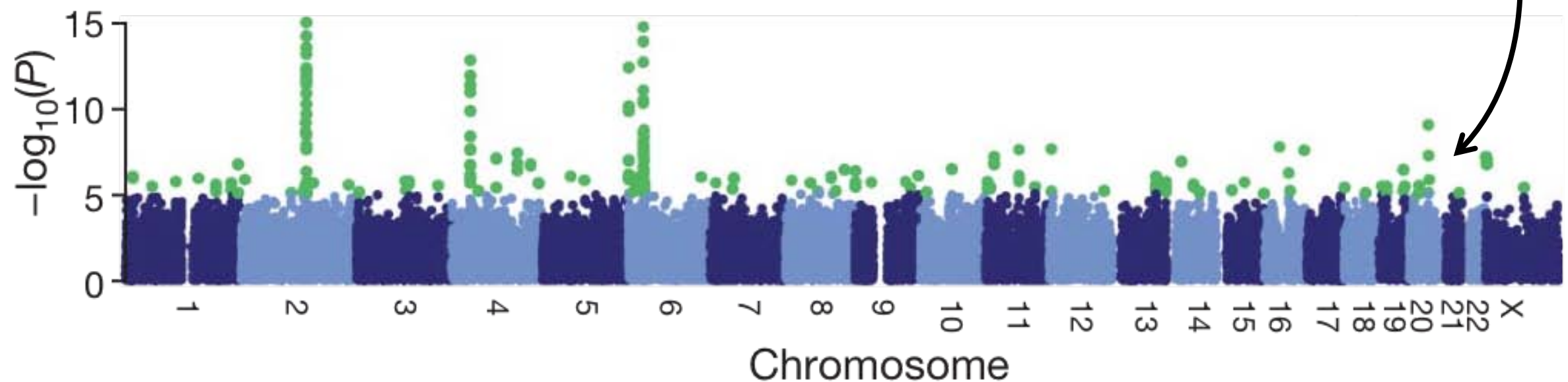


Rappaport S, Smyth M. Environment and Disease Risks.

Science (2010) vol. 330 (6003) pp. 460-461

# Genome-Wide Association Studies (GWAS)

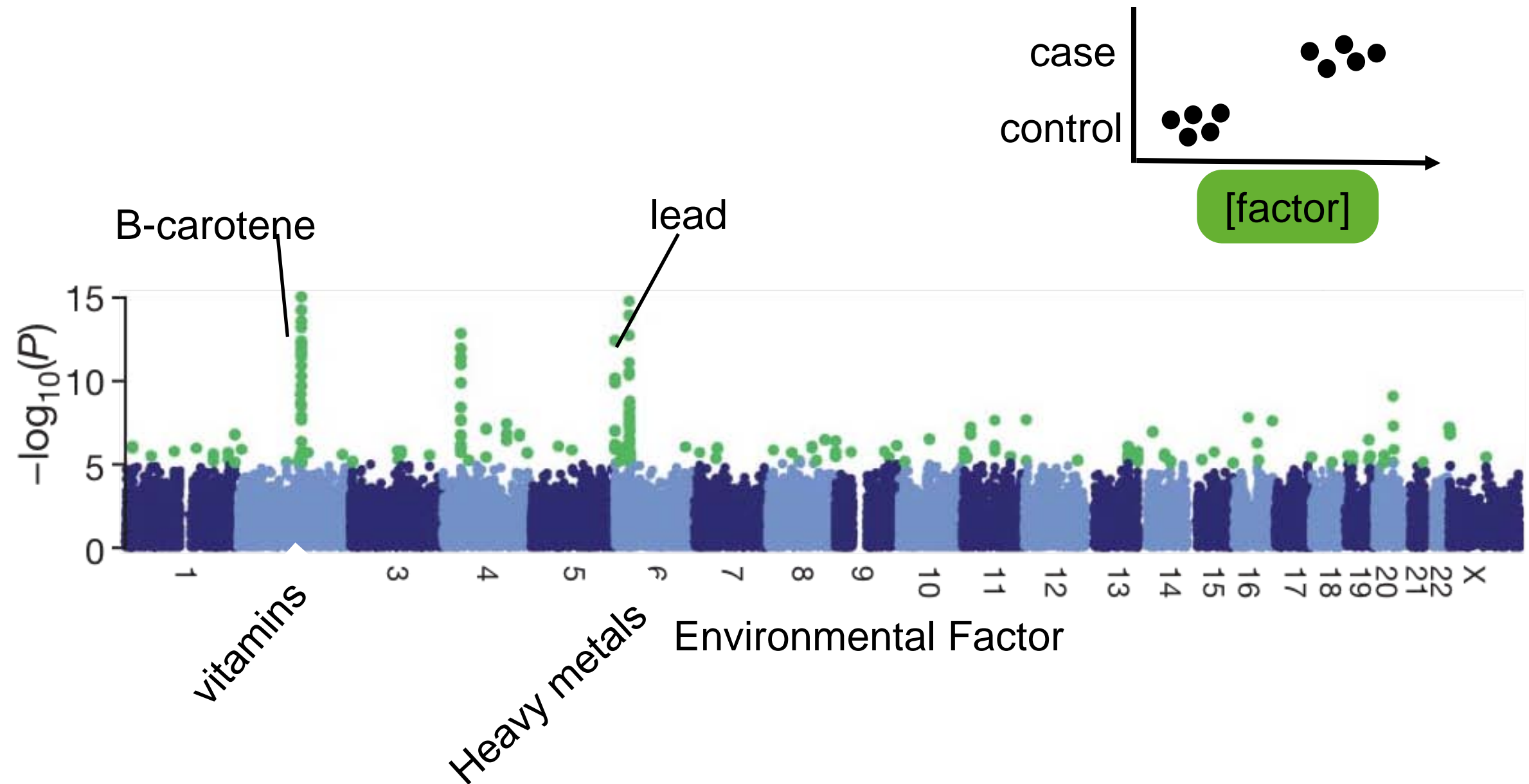
	AA	Aa	aa
case			
control			



~100,000 - 1,000,000 association tests

What specific genetic loci are associated to disease?

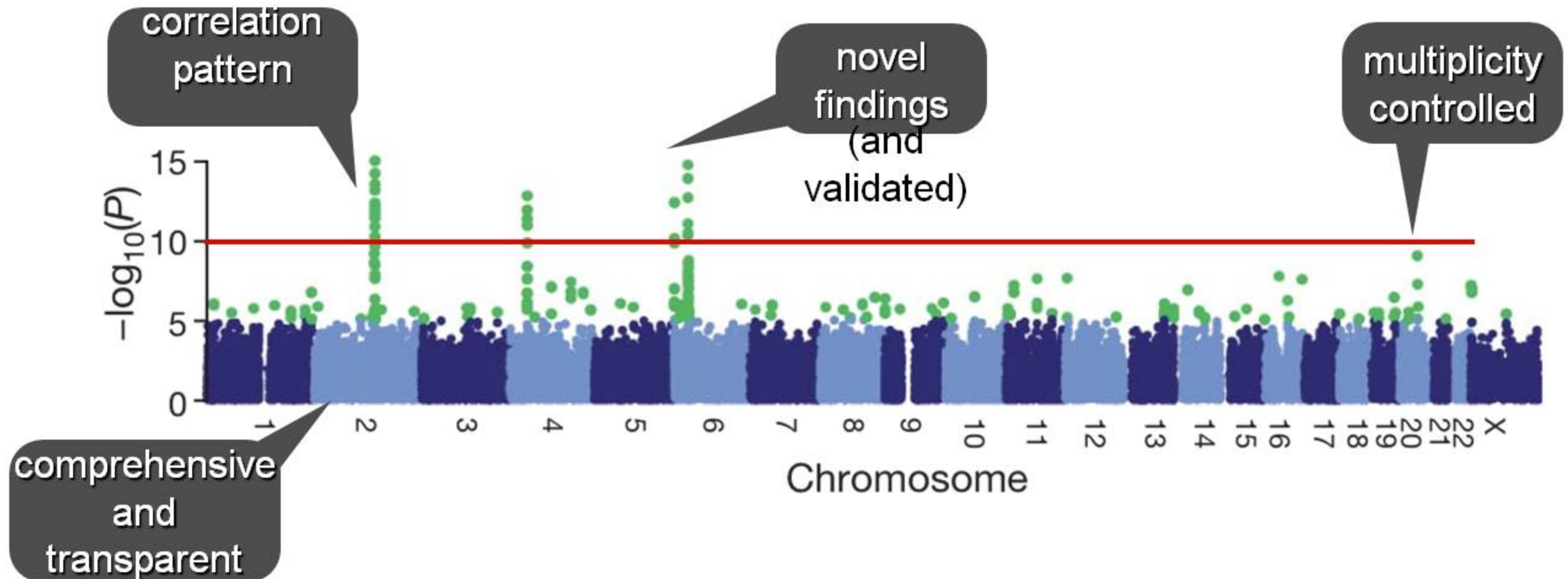
# Environment-Wide Association Studies (EWAS)



What specific **environmental** “loci” are associated to disease?:  
ie, T2D, lipid levels, obesity, etc?



# Why “EWAS”?



Potential for agnostic, comprehensive, and systematic association studies

*However:* confounding & reverse causality bias are multiplied

# NHANES Measurements

## Environmental “E-Loci” Chip



Demographics (N ~10,000)	Examination (N ~ 3000)
Age Sex Income Education Ethnicity	Blood Pressure Body Measurement Diet & Nutrient Intake Vision Oral Health
	Questionnaire (N ~10,000)
Laboratory (N ~ 3000)	
Biochemistry: Triglycerides, cholesterol, glucose, Cl, Na, K, PSA, etc. <div style="background-color: #d9ead3; padding: 10px; margin: 10px 0;"> <b>Exposures:</b>            Heavy metals, dioxins,            PCBs, phenols,            phthalates;         </div> Infectious Diseases Allergens	Disease & Health Status  Drug use  Physical Activity Health & Fitness History  Occupation

Cohorts:  
 1999-2000  
 2001-2002  
 2003-2004  
 2005-2006

Restricted-use:  
 genetic  
 variants!

# EWAS Methodology

Disease status  
Classification

## B Disease Phenotypes

Fasting Glucose  
> 125 mg/dL?  
N=109-3190  
(8% of total)

log10(trigly.)  
N=109-3618

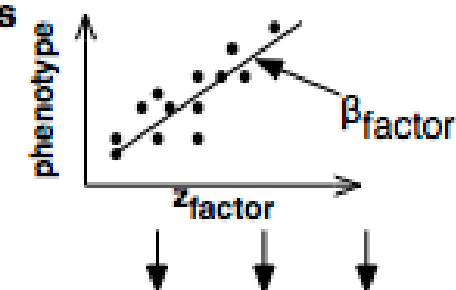
log10(LDL)  
N=101-3368

log10(HDL)  
N=222-7485

Linear Modeling

## C Screening For Disease-associated Factors

$z_{\text{factor}}$  = transformed  $x_{\text{factor}}$   
- age, age\*age, sex, ethnicity, BMI, SES



## D Validation

Empirical FDR estimation  
Permute Phenotype Levels 1000x  
FDR( $\alpha$ )  $\leq$  10%  
→ P-value( $\beta_{\text{factor}}$ ) <  $\alpha$  in 2 or more cohorts?

## A Number of Factors Per Class

	1999-2000	2001-2002	2003-2004	2005-2006
Acrylamide	0	0	2	0
Allergen Test	0	0	0	20
Bacterial	8	13	17	1
Cotinine	1	1	1	1
Diakyl	7	7	6	0
Dioxins	5	7	7	0
Furans	5	5	9	0
Heavy Metals	18	18	23	25
Hydrocarbons	14	22	21	0
Latex	1	0	0	0
Carotenoid Nutrients	0	6	15	7
Mineral Nutrients	2	2	2	1
Vitamin A	3	3	3	3
Vitamin B	4	4	5	3
Vitamin C	0	0	1	1
Vitamin D	0	1	1	1
Vitamin E	2	2	3	2
Polychlorinated Biphenyls	23	26	38	0
Perchlorate	0	0	2	0
Pesticides, Atrazine	0	0	5	0
Pesticides, Carbamate	0	0	1	0
Pesticides, Chlorophenol	0	0	1	1
Pesticides, Organochlorine	10	13	11	0
Pesticides, Organophosphate	2	2	2	0
Pesticides, Pyrethroid	1	1	1	0
Phenols	15	11	9	12
Phthalates	7	12	12	0
Phytoestrogens	6	6	6	0
Polybrominated Ethers	0	0	12	0
Polyfluorochemicals	0	0	10	12
Virus	6	6	10	6
Volatile Compounds	29	14	22	0
<i>total</i>	<b>169</b>	<b>182</b>	<b>258</b>	<b>96</b>

Environmental Factor "Classes"

Factor "class"

"Validation"

# EWAS Methodology, cont'd

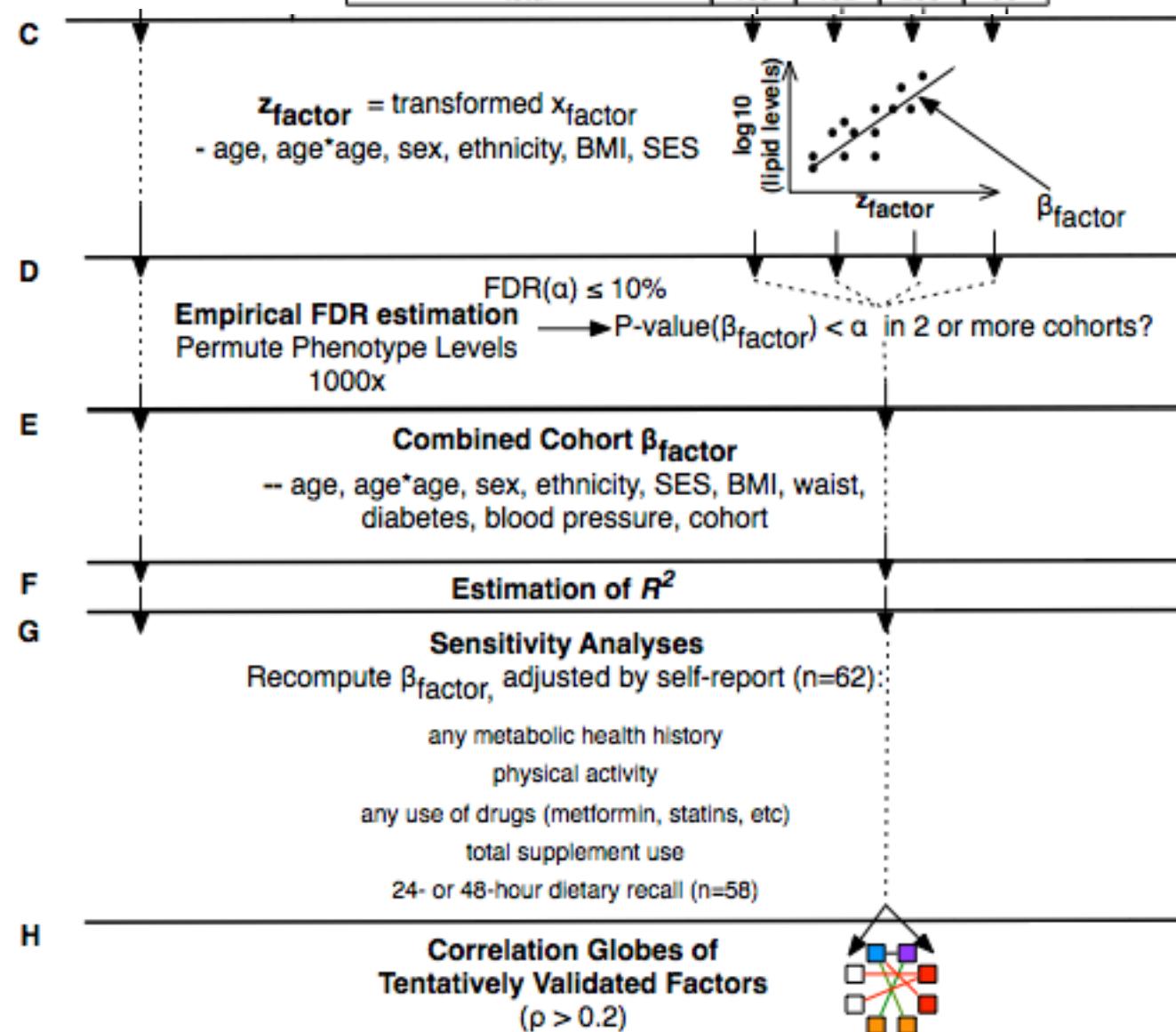
Pesticides, Chlorophenol	0	0	1	1
Pesticides, Organochlorine	10	13	11	0
Pesticides, Organophosphate	2	2	2	0
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Linear Modeling

Empirical False Discovery Estimation

Sensitivity analyses:  
adjust for additional  
factors

Correlation globes





# EWAS on T2DM

cohort markers  
 1999-2000 ◆  
 2001-2002 ■  
 2003-2004 ●  
 2005-2006 ▲

## “Novel” Findings:

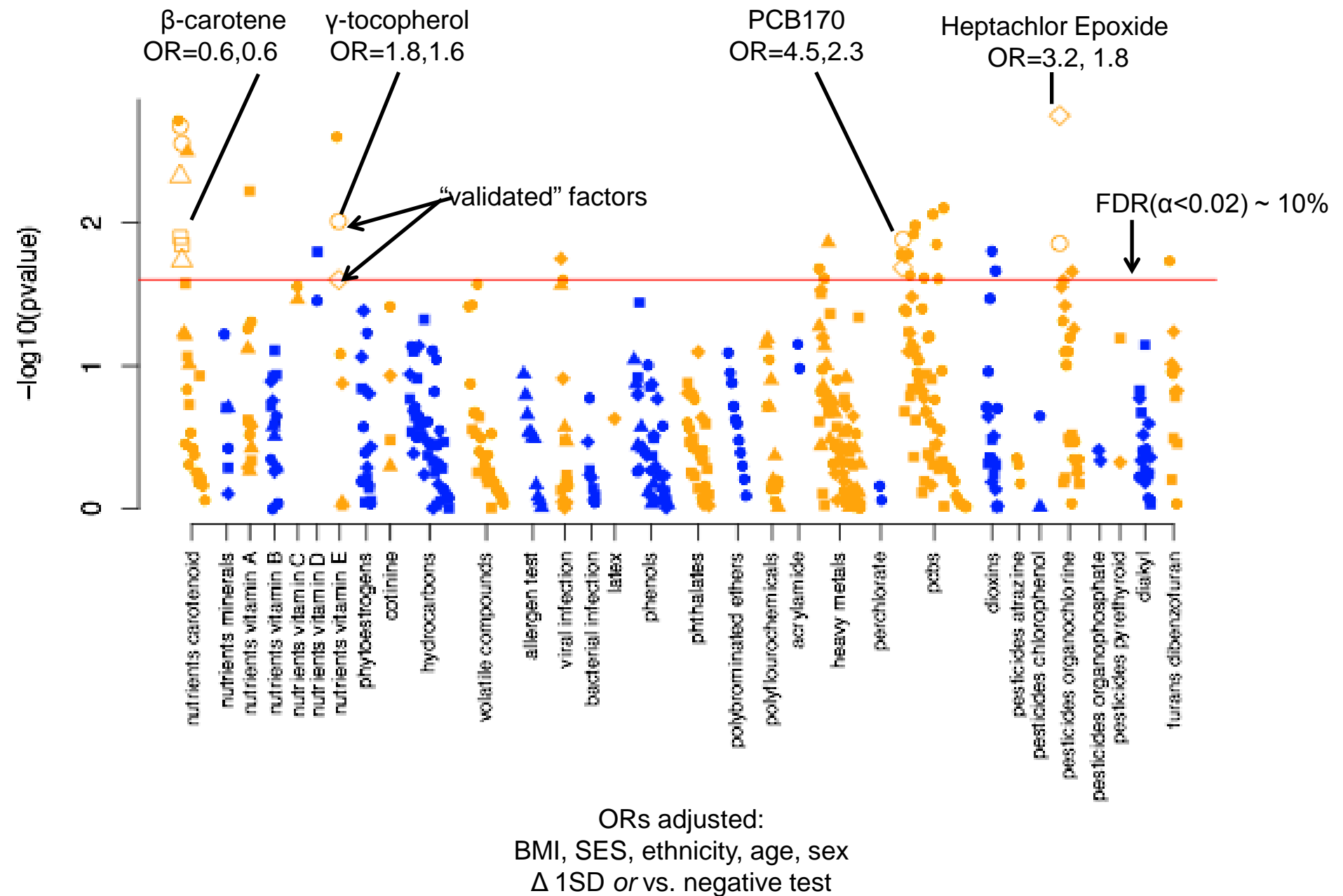
heptachlor  
 γ-tocopherol

## Known Associations:

β-carotene  
 vitamin D  
 PCBs

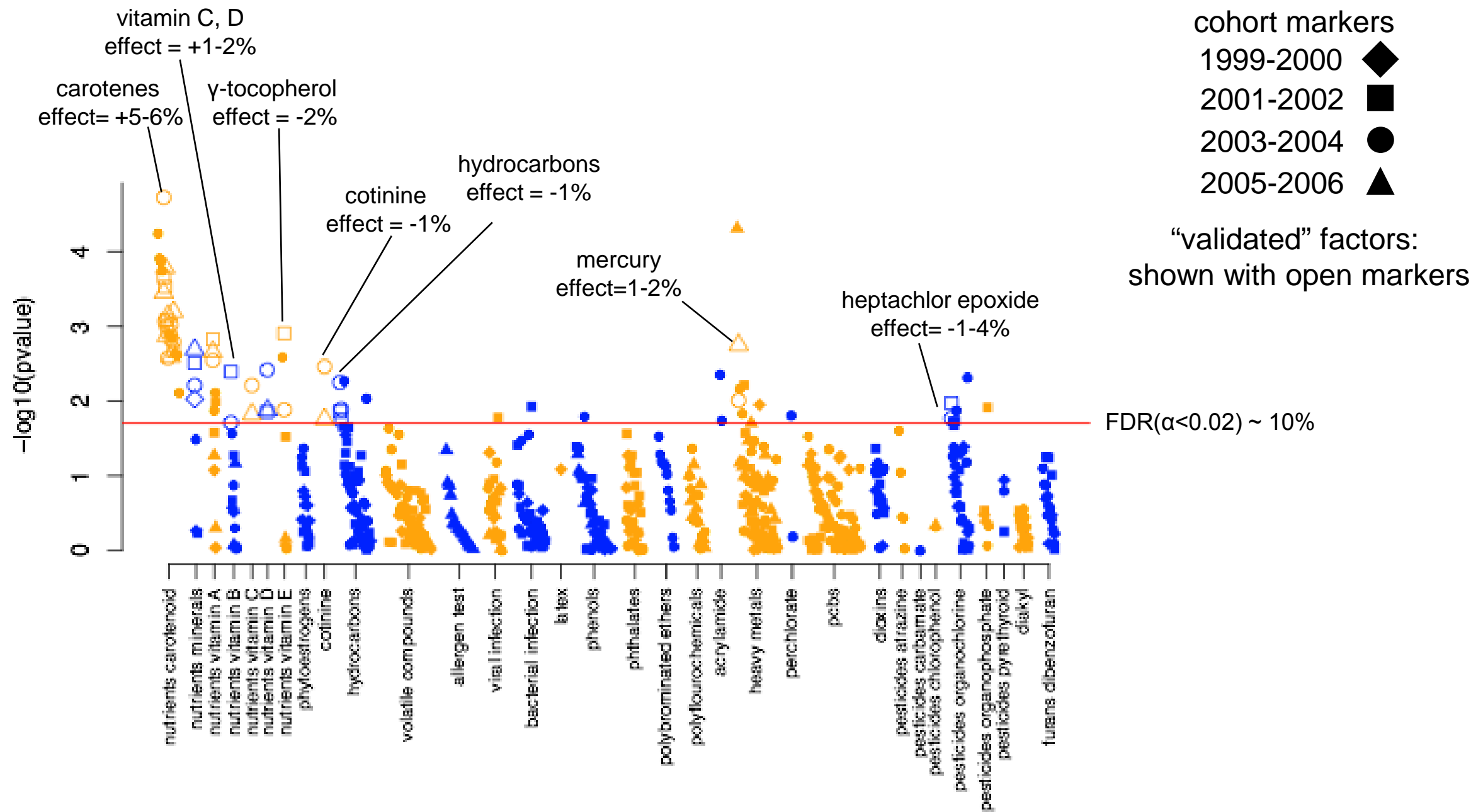
## Interesting Patterns:

dioxins, pesticides,  
 PCBs



What about other risk phenotypes?

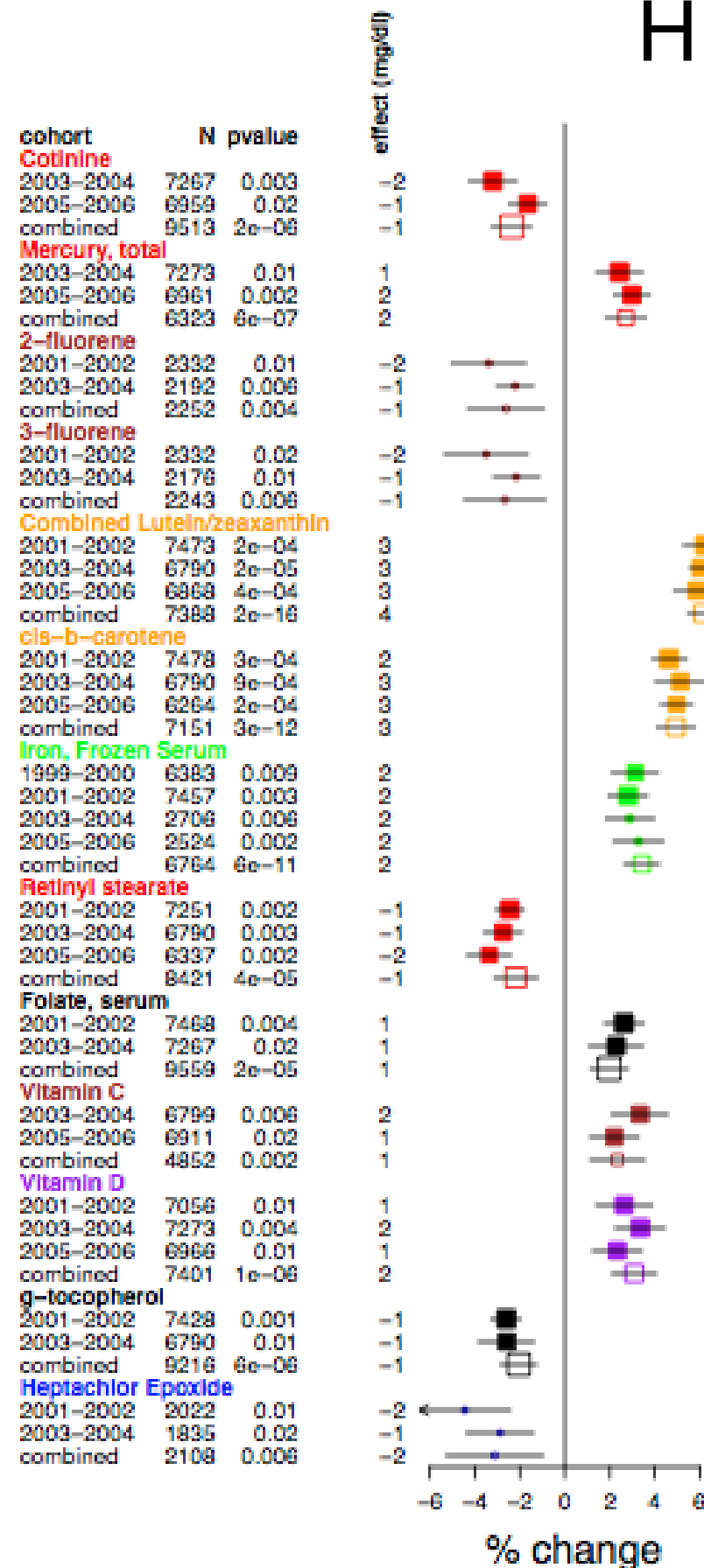
# EWAS on HDL-C



adjusted for:  
BMI, SES, ethnicity, age, age<sup>2</sup>, sex  
effect = %  $\Delta$  for  $\Delta$  1SD or vs. negative test

Patel CJ, Cullen MR, Ioannidis JAP, J, Butte AJ, (2010). Non-genetic associations and correlation globes for determinants of Lipid Levels: an EWAS. In review.

# Effect Sizes For Validated Factors: HDL-C



single cohorts adjusted for:  
BMI, SES, ethnicity, age, age<sup>2</sup>, sex  
effect= %  $\Delta$  for  $\Delta$  1SD  
FDR ~ 10%

‘combined’ adjusted for:  
BMI, SES, ethnicity, age, age<sup>2</sup>,  
sex, blood pressure, cohort,  
diabetes, waist circumference  
effect= %  $\Delta$  for  $\Delta$  1SD  
FDR < 1%

# “Assessing” Bias from Self-Report Data

“source” of bias	examples
disease status	diabetes, CHD, heart attack
drug use	metformin, statins
supplement use	count of total supplements
physical activity	metabolic equivalents
recent food intake	total nutrients

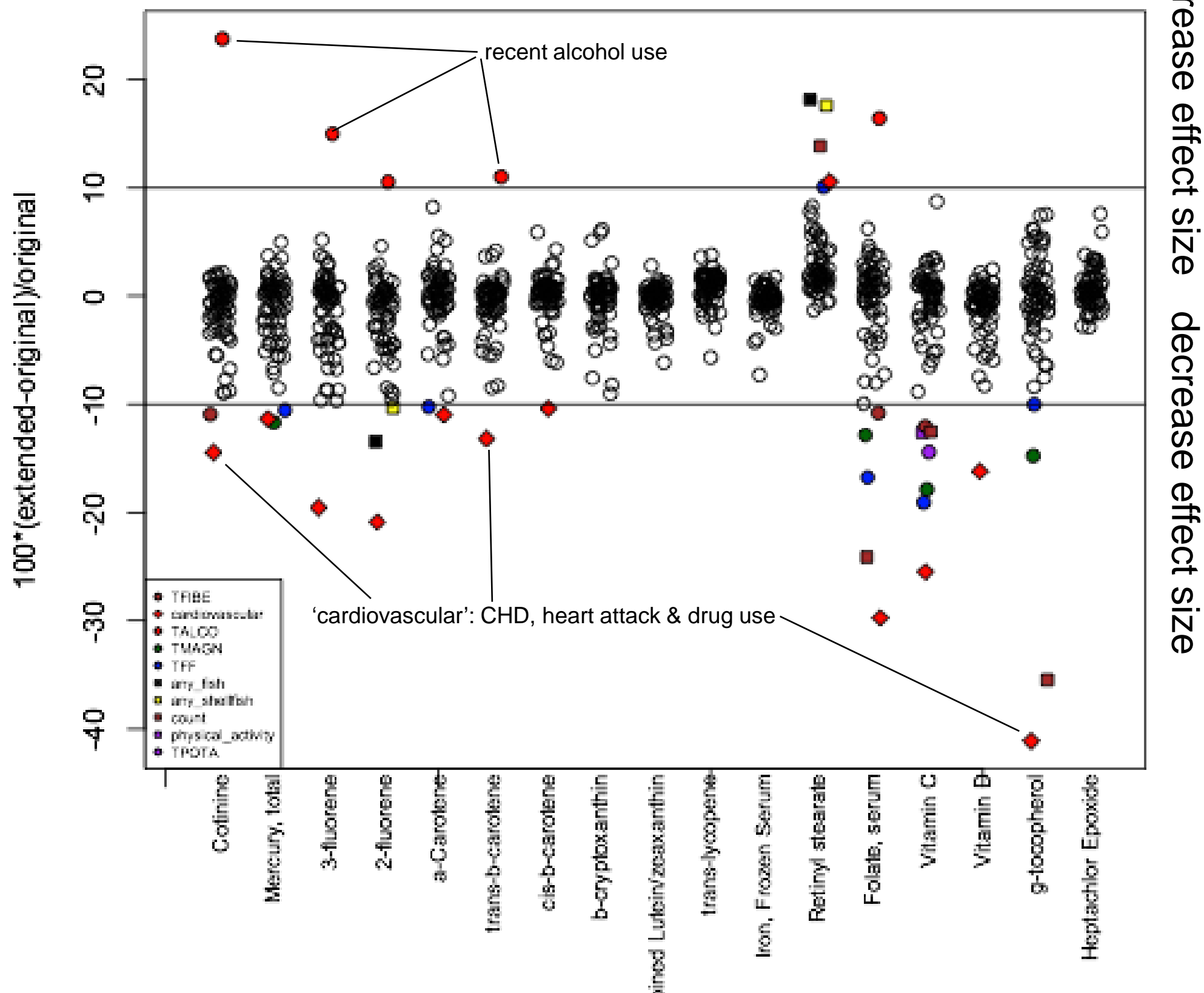
total:62

self-report data are sequentially added to final model  
effect sizes for environmental variable are compared



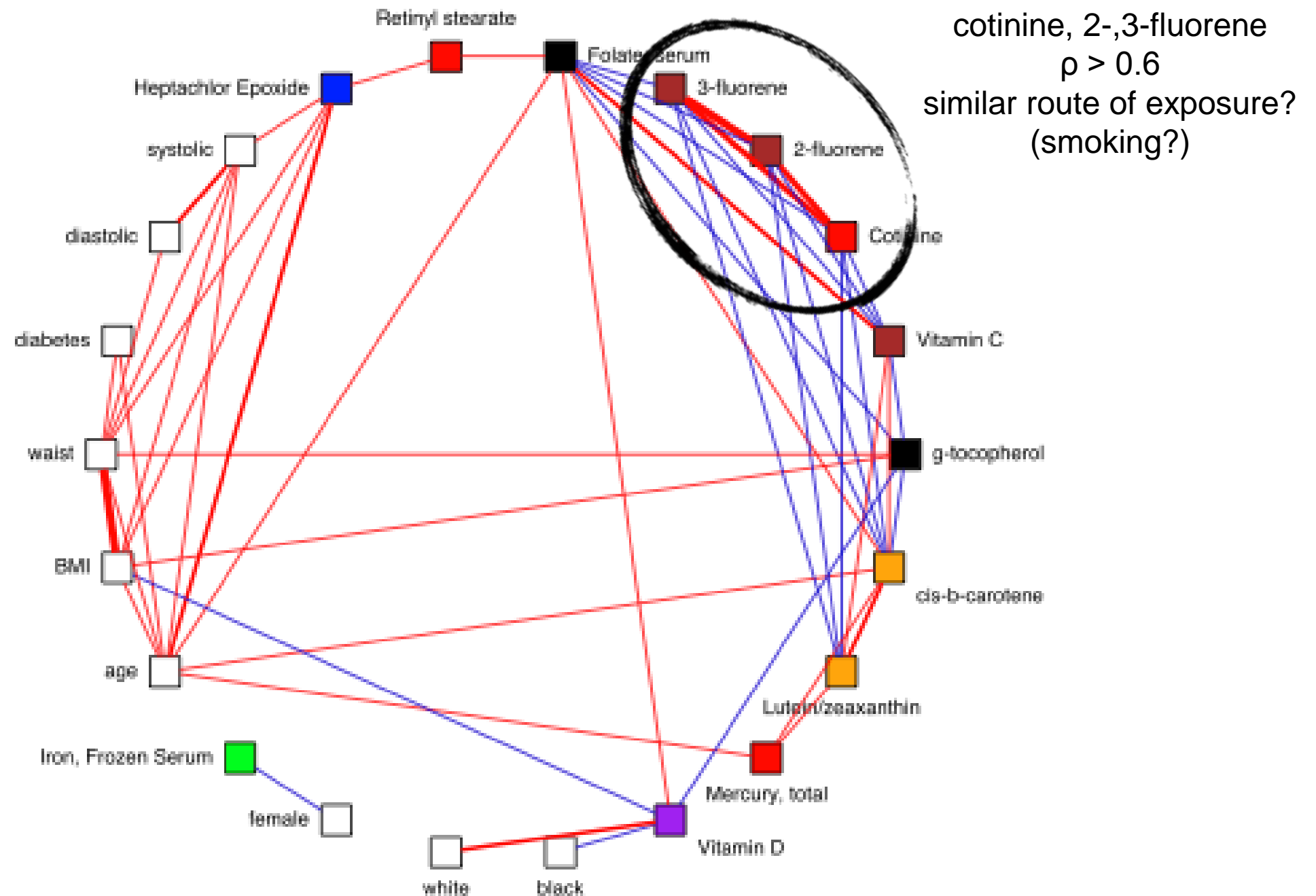
# Assessing Bias from Self-report data

## Factors Validated for HDL-C



# HDL-C “Correlation Globe”

## Dependencies of Validated Factors



# What's next?

Validation: longitudinal studies & model systems

Genome-wide by exposome-wide studies

# Missing Heritability\*: Genome meets Exposome

Variants ascertained from genome-wide studies  
have described little disease variability  
Type 2 Diabetes: 6% (18 loci)  
HDL-Cholesterol: 5% (7 loci)



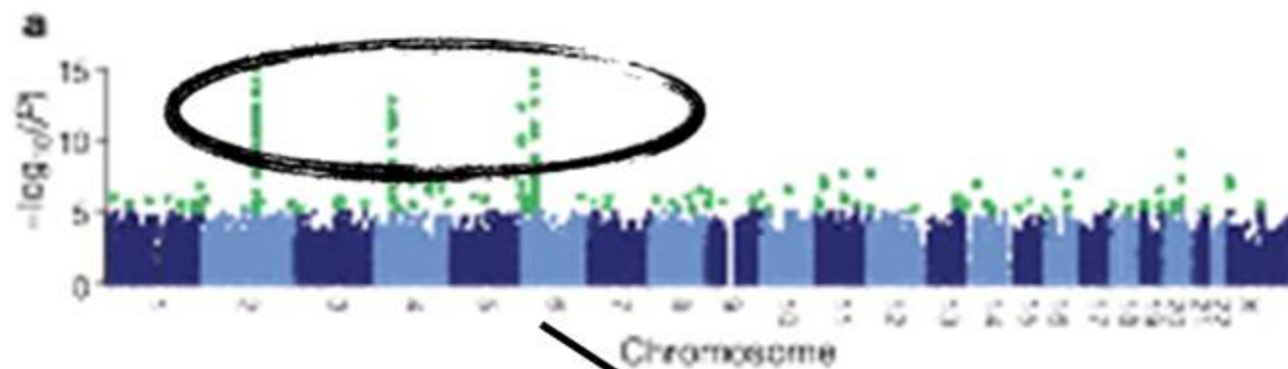
Considering genome in *combination* with exposome might give a better estimate of heritability

\*Manolio T et al. Finding the missing heritability of complex diseases. Nature (2009) vol. 461 (7265) pp. 747

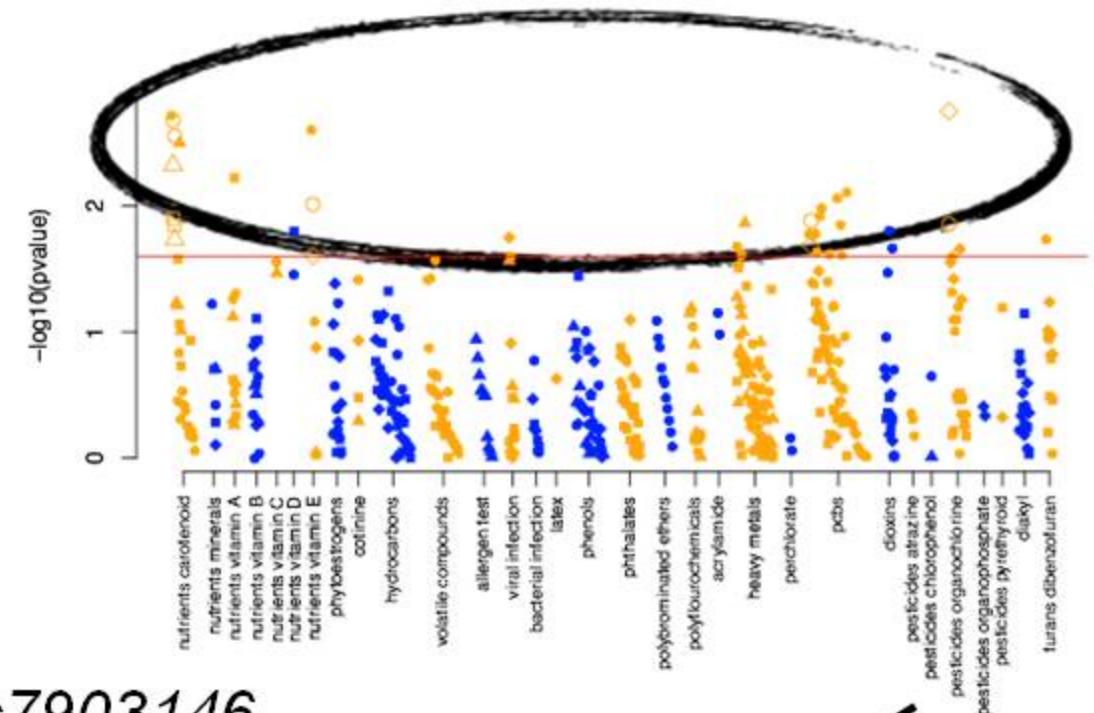
Do known disease-associated genetic variants  
interact with environmental factors found in

EWAS?

Example: Type 2 Diabetes



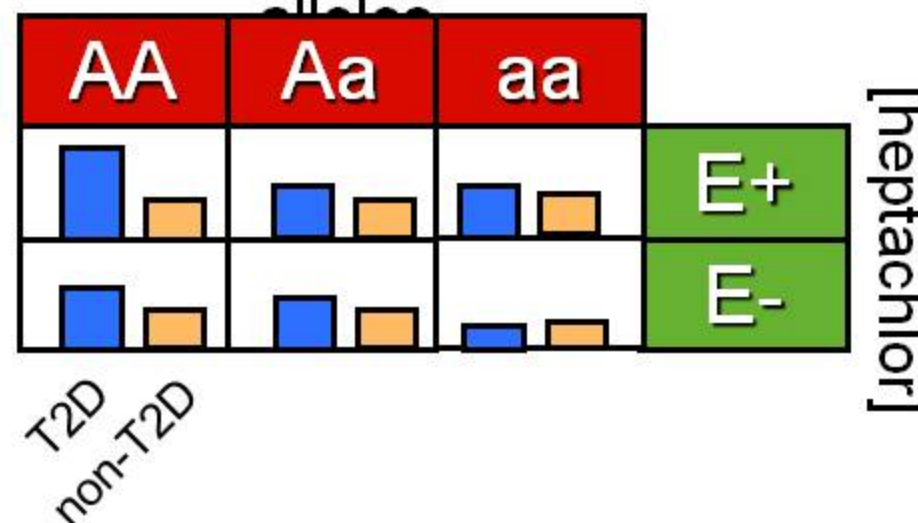
GWAS



EWAS

To test:  
NHANES: 1999-2003  
~ 100 loci associated to  
metabolic related disease (T2D,  
BMI, lipids)  
N ~ 3000

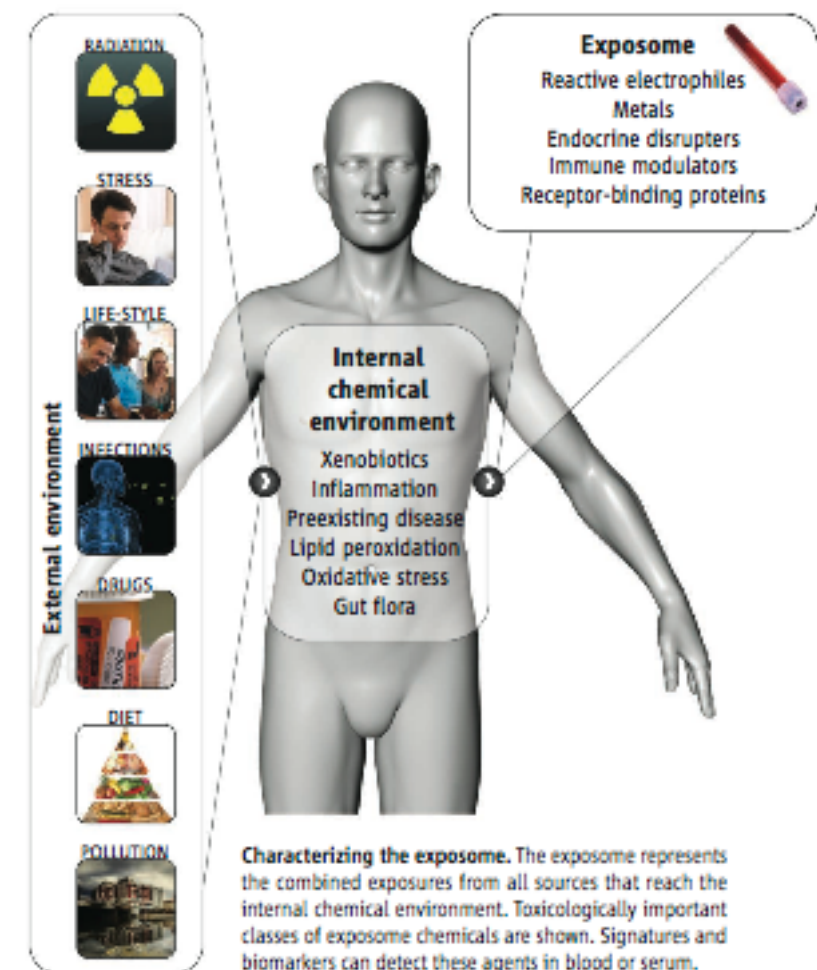
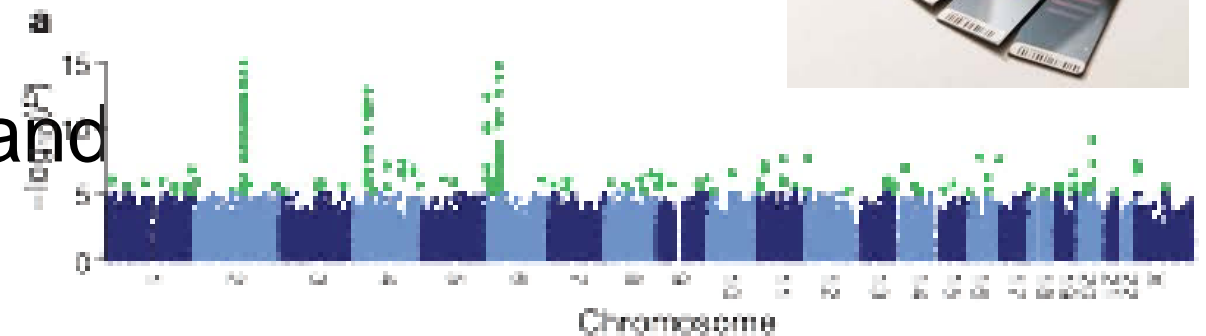
*TCF7L2* rs7903146  
number of risk





# Conclusion and Discussion: EWAS and the “exposome”

- Comprehensive, transparent, and systematic
- *However:* reverse causality, confounding amplified
- Need to define, characterize, and make accessible the “exposome”



# Acknowledgements & Thanks

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Questions?

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**Butte Lab**  
Stanford Center for Biomedical Informatics Research